0/24



# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	10/081,739	
Source:	O IPE	
Date Processed by STIC:	1/29/03	

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<a href="http://www.uspto.gov/ebc/efs/downloads/documents.htm">http://www.uspto.gov/ebc/efs/downloads/documents.htm</a>, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
- 3. Hand Carry directly to:
  - U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
  - U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
- 4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 10 081,739
ATTN: NEW RULES CASES	: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
0 / Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
1Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
3Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001



OIPE

### RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/081,739

DATE: 01/29/2003 Erros (m fl. 3-5

TIME: 08:12:35

Input Set : A:\09010-107001.txt

```
4 <1105 APPLICANT: Callen, Walter
              Richardson, Toby
              Frey, Gerhard
      6
      7
             Miller, Carl
             Fazaoka, Martin
      8
      -9
             inort, cay
             Mathur, Eric
     12 <120: TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
             AND METHODS OF USE THEREOF
     15 <130: FILE REFERENCE: 09010-107001
     17 <140> CUEFENT APPLICATION NUMBER: 10/081,739
C--> 18 <141> CURRENT FILING DATE: 2003-01-21
     20 K150: FRICE APPLICATION NUMBER: 60/270,495
     21 <151: FRICE FILING DATE: 2001-02-20
     33 <150% IRIGE APPLICATION NUMBER: 60/270,496
     24 <1310 FRICE FILING DATE: 2001-02-21
     16 <1800 FRICE APPLICATION NUMBER: 60/291,122
     27 <1510 FRIOR FILING DATE: 2001-05-14
     29 K160: NUMBER OF SEQ ID NOS: 69
     11 <170 FORTWARE: FastSEO for Windows Version 4.0
     \pm 3 <2100 MEQ ID NO: 1
     34 <211: !FNGTH: 1311
     33 KRIZE TYPE: DNA
     36 <2130 (EGANISM: Artificial Sequence
     38 <2360 FEATURE:
     39 <2233 (THEF INFORMATION: Synthetically generated
     41 <4000 SEQUENCE: 1
                                                                                 60
     40 atogecaact anticogacet ogaaaagoge ggggteataa tgeaggegtt etaetgggae
                                                                                120
     43 qtqccttcaq qaqqaatatq qtqqqacaca atacqqcaqa aqataccqqa qtqqtacqat
                                                                                180
     44 genagaatet engesaatatg gatteeened gegageaagg geatgggegg egectatieg
     45 atogqotacq acceptacqa officittidae officgqtqagt acgaecagaa gggaacggta.
     45 gagacgoget tiggotocaa geaggagete gigaacatga taaacacege ecaeggetat
     47 aqqatqaada taataqooqa tataqtosto aaccadegeq eeggeqqtqa eetggagtqq
                                                                                360
                                                                                420
     48 aaccection tgaacgasta tacctggaco qactictoaa aggtegeqto gggtaaafac
     4) acogeoaact acotogacti chacooquae qagotocatq coggogatto oggaacatti
                                                                                480
     50 ggaggotato regacataty chaegacaad ayotgggach agtactggot etgggecage
                                                                                600
     51 caggagaget acgeggeata fotoaggage atoggeatog atgeotiggeg ottogactac
                                                                                660
     52 głnaagggot algeteectą ggregteaag gaetggetga actgglegdq aggetgggeq
                                                                                720
     53 gtiggagagt untgggaran naangingan golgithina anliggghata hingagoggt
     64 gecaaggist tigacti ge shistanfan aagatggatg aggeettiga caacaaaaac
     55 aftocagogn fingbotofyn nyfboagaan gghoagaetg flybotheng igadoceffti
                                                                                940
                                                                                900
     The adoptication contitutings dialocategue acceptation totiggiasion gitationages.
                                                                                960
     57 facqqqttqa finetqachta cqaqqqqqaq neqaqaatat fictacqqqqa etacqaqqaq
```

RAW SEQUENCE LISTING DATE: 01/29/2003 FATERT APPLICATION: US/10/081,739 DATE: 08:12:35

Input Set : A:\09010-107001.txt

58 tygetcaaca aggataaget caagaacete atetggatae atgagaacet egeoggagga 59 ageacegaca tagtetaeta egataacgat gaacteatet tegteaggaa eggetaeggg 63 gacaageegg ggettataac etacatease etaggetega geaaggeegg aaggtgggtt 61 tatgtgeega agttegeggg egegtgeate caegagtata etggtaacet eggaggetgg 62 gtagacaagt acgtetaete aageggetgg gtetateteg aagetecage tracgaceet 63 gecaacegge agtatggeta eteegtgtgg agetactgeg gggtgggetg a 65 <210> SEQ ID NO: 2 66 <211> LENGTH: 436 67 <212> TYPE: PRT 6+ <213> ORGANISM: Artificia. Sequence 60 <220> FEATURE:	1020 1080 1140 1200 1260 1311
71 <223> OTHER INFORMATION: Synthetically engineered	
Tr <400> SEQUENCE: 2	
- 74 Met Ala Lys Tyr Ser Glu Leu Glu Lys Gly Gly Val Ile Met Gln Ala - 74 - 1 - 5 - 10 - 15	
To Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg  20 25 30	
The Glr. Lys lie Pro Glu Trp Tyr Asp Ala Giy Ile Ser Ala Ile Trp Ile 39 40 45	
80 Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp 81 50 55	
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Glr Lys Gly Thr Val -+: 65 75 80	
65 70 70 70 70 70 70 70 80 80 80 80 80 80 80 80 80 80 80 80 80	
ce Ala His Ala Tyr Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His	
fr Arg Ala Gly Gly Asp Leu Glu Trp Ash Pro Phe Val Asr Asp Tyr Thr	
to Trp Thr Asp She Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Ash Tyr 135 140	
19. Leu Asp Phe His Pro Asm Glu Leu His Ala Gly Asp Ser Gly Thr Phe 23 145 150 158 160	
4 Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gir Tyr Trp 165 170 175	
10 Let Trp Ala Ser Gir Glu Ser Tyr Ala A.a Tyr Let Ard Ser Ile Gly 180 185 190	
35 lie Asp Ala Trp Arg Phe Asp Tyr Va. Lys Gly Tyr Ala Pro Trp Val 9 · 195 200 20!	
100 Val Lys Asp Trp Leu Asn Trp Trp G.y G:y Trp Ala Val Gly Glu Tyr 101 210 215 220	
102 Trp Asp Thr Ash Val Asp Ala Val Leu Ash Trp Ala Tyr Ser Ser Gly 103 225 230 235 240	
104 Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe	
106 Asp Ash Lys Ash lie Pro Ala Leu Val Ser Ala Leu Gln Ash Gly Gin	
107	

#### RAW SEQUENCE LISTING

HATENT AFFLICATION: US/10/081,739

DATE: 01/29/2003 Time: 08:12:35

Input Set : A:\09010-107001.txt

```
110 His Asp Thr Asp lie lie Trp Ash Lys Tyr Pro Ala Tyr Ala Phe lle
        290
                             295
112 Lea Thr Tyr Slu Gly Gln Fro Thr ile Fhe
                        310
11: Trp Leu Ash Lys Asp Lys Leu Lys Ash Leu Ile Trp Ile His Glu Ash
                     325
                                          330
115
116 Les Ala Sly Sly Ser Thr Asp 11e Val Tyr Tyr Asp Ash Asp Slu Leu
11'
                340
                                                          350
118 lle Phe Val Ary Ash Gly Tyr Gly Asp Lys Fro Gly Leu lle Thr Tyr
            355
                                 360
11+
                                                      365
120 Ile Ash Leu Gly Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
        370
                             375
1... Phe Ala Gly Ala Cys IIe His Glu Tyr Thr Gly Ash Leu Gly Gly Trp
1.13 335
                         390
                                             395
1.4 Val Asp bys Ty: Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                    405
                                         410
1.6 Ala Tyr Asp Pro Ala Ash Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
                4.20
                                     425
                                                          430
1. - Cys Bly Val Bly
1.:+
    435
                                       Invalid response, see ever summing
Sheet item 10
1:1 < 210 + SEQ ID 10: 3
1 . <.!!! LENGTH: 1419
1 to <212 · TYPE: DNA
1:4 <213 - ORGANISM: (Environmental
1.4 <400 - SEQUENCE: 3
10^{\circ} augurential territitit gescaetgee tegetgitet gescaacagg abageoegee
                                                                              60
1.1 auggetgeog cabigettaa oggbaccatg atgbagtatt tigaatggta cityboggat
                                                                             120
15^{\rm th} gatgycaegt takippaeeaa agtgyceaat qaageeaaea asttateeag eettgyeate
                                                                             130
140 alegetettt ggingeegee egettacaaa ggaacaagee geagegaegt agggtaegga
                                                                             240
141 ghatacquot tghatgacch oggogaatto uatbauaaaag ggaccgtoog cacaaaatac
                                                                             300
142 gyaabaaaag of Matatot toaagooatt caagoogoob acgoogotgg aatgoaagtg
                                                                             360
143 tucgocgatg togrigttoga coataaaggo ogogotgacg goabggaatg ggtggacgoc
                                                                            4.20
144 ghegaagtea at Higtoega eegbaaceaa gaaatetegg geabetatea aatbbaagea
                                                                             480
145 tygangaaat ttynttttee egggegggge aanaectaet eeagettiaa gtggegetgg
                                                                             540
146 taccatttig acgregitiga tigggacqaa agsegaaaat tigageegeat titasaaatte
                                                                             600
14" ogoggoatog goaaagogtg ggattgggaa gtagacangg aaaacggaaa ctatgactac
                                                                             660
148 ttaatgtatg cogacettga tatggateat coogaagteg tgacogaget gaaaaactgg
                                                                             720
149 qqqaaatgqt atqtcaacac aacqaacatt qatqqqttcc qqcttqatqc cqtcaaqcat
150 attaagitka gittititika igatiggiiq tagtatqiga gitataagaa iggcaagaag
                                                                             840
                                                                             900
151 ctatttaccq toggggaata tiggagofat gacatcaaca agiigcacaa tiacattacg
152 aaaacaqacg gaacgatgic titgtiigat gecoogitac acaacaaati tiataccgci.
                                                                            960
153 tocaaatdag ggggggdatt fgatatgdgd acgttaatga ccaatactot catgaaagat
                                                                            1020
154 caaccgacat tggcogtoac ottogttdat aatcatgaca oogaaccogg ccaagcgctg
                                                                            1080
15% cagtoatggg tingacocatg uttoauaring tiggottaing cottitation aactoggrag
                                                                            1140
156 qaaggataco ogtgogtott tiatggigad tattatggca tiocadaata taadattdot.
                                                                            1200
157 tegetgaaan geaaaategn teegeteete ategegegegen gggattatge ttaeggaaeg
158 caadatqatt atottgatca ctoogarafo atoggqtqqa caaggqaaqq gqtoacfqaa.
159 adappagnat cogggotydo ngbactydth abbgatyyyn ogggagyddd baaatgdaty
                                                                           1380
100 tactigtt pin aaacaababg otggaaaagt gitolatga.
                                                                            1411
```

#### RAW SEQUENCE LISTING

FATENT APPLICATION: US/10/081,739

DATE: 01/29/2003 TIME: 08:12:35

Input Set : A:\09010-107001.txt

```
162 <210 SEQ ID NO: 4
1.3 <211 - LENGTH: 1539
164 <012 - TYPE: DNA
165 CO13 · ORGANISM: Environmental
16 1 0400 + SEQUENCE: 4
                                                                               6.11
10-10ga absac salaabyget ttacycooga ttyctgacyc tyttatttyc getcatetto
100 tigorgooto attotypago agogyogyda aatottaaty gyadgotgat goaytattii
                                                                              1. 0
                                                                              1: \epsilon
17 platigiada igodosatga oggodaadat tggaagogot tgdaasadga otoggdatat
                                                                              241
17) trigg-tgaad adigstattae tgoogtotgg attocooogg datataaggg aabgagcoaa.
                                                                              31.1

    pegg:tgtgg go:acggtgb ttabgacott tatgatttag gggagtttca tcaaaaaggg.

                                                                              2001
17- neggitoogga dalagtaogg cacaaaagga gagotgcaat otgogatoaa aagtottoat
                                                                              4.0
174 thochodada tiliabqittia oqqqqatqiq qibatbaaqo abaaaqqqqq oqqiqatqoq.
17^{\circ} -coogdagaty takoogogyt tgaagtogat boogbtgabb gbaacogogt aatttbagga
                                                                              4200
                                                                              540
17) quaducegaa tthaaqeetg gadadatttt cattttoogg ggogoggdag cadatadage
197 yulin bawat gighalliggta biattitigab ggaabogatt gggabgagto oogaaagotg
17^{\circ} Habbaratot atHagtttoa aggasaggot tgggattggg aagtttocas tgsssacggd
                                                                              Fift)
                                                                               7. 0
179 Wadtatgatt athigatgia tgoogabato gattatgado atootgatgi ogbagdagaa
                                                                              7200
1-0 Attaugagat ggggbacttg gtatgobaat gaabtgbaat tggaoggttt bogtbttgat
                                                                              840
1-1 quogressas abuttasatt toottotttg ogggattggg titaatoatgt cagggassas
                                                                              特色色
1-1 anggagaagg aawtgtttac ggtagotgaa tattggcaga atgacttggg ogogctggaa.
                                                                              9000
1:3 wactiffing admagadage fiftheatout fougfighting admirphospot foutfatheag
                                                                             10.70
1-4 thosatgety batogapaba gggaggoggo tatgatatga ggaaattgot gaabggtabg.
                                                                             1026
10^{-6} Great thoose agreences to grasspositing acattrictor at second second cost.
1-) qqqqqaatogo fityaqtogab tqtodaaaba tqqtitaaqo oqditqoita oqditiboati.
                                                                             11:00
107 btoadaaggg aatotggata bootdaggtt ttbtabgggg atatgtadgg gadgaaagga
168 grothopago gogaaattoo tgoottgaaa babaaaattg aabogatott aaaagogaga.
                                                                             1. 60
169 isaczytatą cynacygago acagbatgat tatttogado accatgadat tytogyctyg
                                                                             13.0
100 emanygaan goyadagoto gyttgoaaat toagytttgg oggdattaat aadanadgga
                                                                             1 ....
191 ordgroggg dalagogaat goatgooggo oggoaaaaog obggogagab atggoatgab
                                                                             1440
                                                                             1 . . . .
1M. Anta oggas songttogga geoggttgto atbasttogg saggettggg sgsgtttbab
                                                                             15 . 4
198 maasoggog ggtoggttto aatttatgtt caaagatag
1^{19} \cdot 4010 \cdot \text{SBQ} \text{ ID NO: } 5
196 HALL LENGTH: 1395
130 HU12 - TYPE: DNA_
1 to + U15 + OEGANISM: Environmental
D + K400 - SEQUENCE: 5
[1] griggtgdada tgaagttgaa gtadettgdd ttagttttgt tggdtgtggd ttdgataggd
                                                                               Est.
. H. orachotoga otocagtiggg tgotgocaag tactoogaac togaagaggg oggtigttata
                                                                               ੍ਰੇ ਤਹ
. 🕩 argonggoot totaotygga tyttooogga gygggaatot gytyggyacac bataagabag
. 👊 amaan.coogg agtggtacga ogotggaato toggogatat ggattootoo agotagoaaa
                                                                              1.1 \pm
it gagatggggg giggttattc catgggctac gatcoctacg atticttiga botoggogag
                                                                               3.11
                                                                               3.61
.i+ tuctutcaga agggaacagt tgagacgcyc ttcggctcaa aggaggaact ggtgaacatg
                                                                              4.10
{\cal N}^{-1} atalacaccy cacactesta tygoataalay ytyataysyg acataytsat alabsacsys
. We groggtggag accettgagtg gaadcoottt gtaaacaact atacttggad agacttotoo
                                                                              4 ...
1:00 auggtogoot coggtaaata cacggocaac tacottgabt tobacbbasa ogaggtbaag
                                                                              €.,+.
210 tectgegaty agggtacatt tygtgacttt coggacatog cocacgagaa gagotyggat
                                                                              6 111
21% cagtactigge tetiggically calatigagage talegological atoticoggag cataggigate
                                                                              6611
                                                                              7.20
21: gatgeatgge gtttegaeta egteaaaggt taeggagegt gggttgttaa tgaetggete
                                                                              730
215 amotggtggg gaggotgggo ogttggagag taotgggada ogaaegttga tgdactdott
```

#### RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/081,739

DATE: 01/29/2003 TIME: 08:12:35

Input Set : A:\09010-107001.txt

```
214 aactgggcat abgacagogy tgbcaaggto tittgactico ogcictacia caagatggac
                                                                                                                              840
                                                                                                                              900
215 gaaq ottitg araacabcaa catooobgot tiggittacg obotobagaa bggaggaaca
                                                                                                                              9.,)
216 ptoqittobo gogatocotti baaqqoaqta acttooqtiq boaaccabga tacagatata 👚
217 atot gaada adtatooggo ttatgogtto atdottadot atgaggada gootgotata
                                                                                                                            10.
.(1) titt koogog abtaogagga gtggotoaac aaggataago ttaacaabot tatotggata
.11% pappagoado trapoggaga aagtaccaaq atoototact acqataacqa tgagotaata
                                                                                                                           1.;
1.27^{\circ} theatqaqqq adqqctaeqq qaqeaaqeeq qqeeteataa estadataaa seteqqaaac =-1.46^{\circ}
.D21 pactyggoog adogotgggt gaabgtoggo toaaagtittg coggotabab aatocatgaa.
                                                                                                                            ] . .,.
                                                                                                                             1 . . .
.1. Lacadaggea atorogytyy otygyttyae aggtygytte agtacyatyy atgyyttaaa
                                                                                                                            1 ...
... rganggdad otdobbatga todagodaab ggatattabg gotadtdagt otggagotab
                                                                                                                             1 - 41
ul. 4 goaquoqtog gatga
11.46 -12.10 - SEQ ID NO: 6
HEV 4H11 - DEMGTH: 1386
HOW WHILE TYPE: DNA
... + KU15 + ORGANISM: Bacteria
331 - 300 - SEQUENCE: 6
Him ungangaagt stytogooot gotoataacc atgottotog tagogagoat ggcagtogto
                                                                                                                               1.0
. No gradugodag otugogodgo aaagtattoo gagotogaag aaggoggogt tataatgoag
리다 questionadt gggaoghood aggraggagga abonggingig acadcatbag gagdaagata.
                                                                                                                               ) BU
                                                                                                                              1.40
. 35 beggaagtqut abgaqqoqqq aatatoogob atttggatto ogobagbbaq baaggggatg
                                                                                                                               \S(0)_{\mathbb{R}}
.:7 caqaaqqqaa ooltogaaac gogotttggo totaaacagg agotcatcaa tatgataaac -
                                                                                                                              - 610
. The angunocating consequest assumpticate geographic tests assocs conjequence .
                                                                                                                              1.11
134 gradscotog agiggaacco gttogotogg gactacacct ggacggactt otcaaaggtg
.30 quotingquia aatataotyo baastaooto qasttooabo obaaqqagqt baaqtgotgt
                                                                                                                              4,40
                                                                                                                              Erroli
141 quoqueggica cautoggagg ottoccagae atagecoacg agaagagetg ggaccageac
PAT in ignictigge ogagogatga gagotaogos gootaostaa ggagoatogg ogttgatgoo
                                                                                                                              FIELD
                                                                                                                              7.4
24) tigorottig actaogigaa gggotaogga gogtgggtog toaaggacig gotosacigg
                                                                                                                              77-1
.744 tagamogget ggmacgtegg oglagtabtgg gadabdaabg titgatgdabt obtbaabtgg
.46 gratuatiqa gagagasaa ggtattagas tidoogatat astacaagat ggatgaggos
                                                                                                                               -- 🚅 T
.4) L'itgacaaca aawacattoo agogotogto totgocotto agaacggoos gaotgtigto
                                                                                                                              +. 1
                                                                                                                              44.1
.47 Leophogaed contoaaqqo oqtaacottt otaqbaaaco acqababoqa tataatotgg
14% ascargianc tipottatgo titoatisto acciacgaag godagoogt cataticiac
                                                                                                                             10.0
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117 H. IOH SEQ ID NO: 7
158 0 11. LENGTH: 472
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260 CLIE GEGANISM: (Environmental)
261 - 1400> SEQUENCE: 7
265 Met Phe Leu Leu Ala Phe Leu Leu Thr Ala Ser Leu Phe Cys Pro Thr
264
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265 G.y Gln Fro Ala Lys Ala Ala Ala Fro Phe Asn Gly Thr Met Met Gln
266
              20
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# VERIFICATION SUMMARY

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EATENT APPLICATION: US/10/081,739

DATE: 01/19/2003 TIME: 08:12:80

Input Set : A:\09010-107001.txt

Output Set: N:\CRF4\01292003\J081739.raw

1:18 M:271 C: Current Filling Date differs, Replaced Current Filling Date